

Serial Number: 10/017,621

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was wrapped down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☒ Deleted extra invalid headings used by an applicant, specifically: 22207 line - seq. 3
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

#2 OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,621

DATE: 01/10/2002

TIME: 20:06:04

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01102002\J017621.raw

3 <110> APPLICANT: Susan M. Freier  
 4 Mark P. Roach  
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION  
 8 <130> FILE REFERENCE: RTS-0350  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/017,621  
 C--> 10 <141> CURRENT FILING DATE: 2001-12-07  
 10 <160> NUMBER OF SEQ ID NOS: 89  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 20  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Artificial Sequence  
 18 <220> FEATURE:  
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 22 <400> SEQUENCE: 1  
 23 tccgtcatcg ctcctcaggg 20  
 26 <210> SEQ ID NO: 2  
 27 <211> LENGTH: 20  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Artificial Sequence  
 31 <220> FEATURE:  
 33 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 35 <400> SEQUENCE: 2  
 36 atgcattctg cccccaagga 20  
 39 <210> SEQ ID NO: 3  
 40 <211> LENGTH: 1745  
 41 <212> TYPE: DNA  
 42 <213> ORGANISM: Homo sapiens  
 44 <220> FEATURE:  
 45 <221> NAME/KEY: CDS  
 46 <222> LOCATION: (124)...(1614)  
 48 <400> SEQUENCE: 3  
 49 tggaagcagc gtaaaggatg gacaggaatg cagaggtagg caggaggacc agcagtgtga 60  
 51 ctgctgaaac ccaggggagg gccccgcggc tctgaggttg ctgcgcgcgc cccgccgatac 120  
 53 gcc atg gat cgg atg aag aag atc aaa cgg cag ctg tca atg aca ctc 168  
 54 Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met Thr Leu  
 55 1 5 10 15  
 57 cga ggt ggc cga ggc ata gac aag acc aat ggt gcc cct gag cag ata 216  
 58 Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln Ile  
 59 20 25 30  
 61 ggc ctg gat gag agt ggt ggt ggt ggc ggc agt gac cct gga gag gcc 264  
 62 Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly Glu Ala  
 63 35 40 45  
 65 ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc cca ctc 312  
 66 Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro Leu  
 67 50 55 60  
 69 agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg tct gat 360  
 70 Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser Asp

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71	65	70	75	
73	ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg cag tct	408		
74	Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln Ser			
75	80	85	90	95
77	cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc tcc act	456		
78	Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser Thr			
79	100	105	110	
81	gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg ctg cct	504		
82	Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu Pro			
83	115	120	125	
85	gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt gac aag	552		
86	Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp Lys			
87	130	135	140	
89	ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att ggc ttt	600		
90	Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly Phe			
91	145	150	155	
93	ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag ggt acc	648		
94	Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly Thr			
95	160	165	170	175
97	tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac ctt gtg	696		
98	Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu Val			
99	180	185	190	
101	gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc tgc acc	744		
102	Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr			
103	195	200	205	
105	gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc aac atc	792		
106	Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala Asn Ile			
107	210	215	220	
109	gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc ctt gtc	840		
110	Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr Leu Val			
111	225	230	235	
113	ttt gag tac ctg gac aag gac ctg aag cag tac ctg gat gac tgt ggg	888		
114	Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp Cys Gly			
115	240	245	250	255
117	aac atc atc aac atg cac aac gtg aaa ctg ttc ctg ttc cag ctg ctc	936		
118	Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu Leu			
119	260	265	270	
121	cgt ggc ctg gcc tac tgc cac cgg cag aag gtg cta cac cga gac ctc	984		
122	Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp Leu			
123	275	280	285	
125	aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag ctg gct	1032		
126	Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala			
127	290	295	300	
129	gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca tac tcc	1080		
130	Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr Tyr Ser			
131	305	310	315	
133	aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg ctt ggg	1128		
134	Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu Leu Gly			
135	320	325	330	335

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137 tcc acg gac tac tcc act cag att gac atg tgg ggt gtg ggc tgc atc      1176
138 Ser Thr Asp Tyr Ser Thr Gln Ile Asp Met Trp Gly Val Gly Cys Ile
139                               340                               345                               350
141 ttc tat gag atg gcc aca ggc cgt ccc ctc ttt ccg ggc tcc acg gtg      1224
142 Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr Val
143                               355                               360                               365
145 gag gaa cag cta cac ttc atc ttc cgt atc tta gga acc cca act gag      1272
146 Glu Glu Gln Leu His Phe Ile Phe Arg Ile Leu Gly Thr Pro Thr Glu
147                               370                               375                               380
149 gag acg tgg cca ggc atc ctg tcc aac gag gag ttc aag aca tac aac      1320
150 Glu Thr Trp Pro Gly Ile Leu Ser Asn Glu Glu Phe Lys Thr Tyr Asn
151                               385                               390                               395
153 tac ccc aag tac cga gcc gag gcc ctt ttg agc cac gca ccc cga ctt      1368
154 Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro Arg Leu
155 400                               405                               410                               415
157 gat agc gac ggg gcc gac ctc ctc acc aag ctg ttg cag ttt gag ggt      1416
158 Asp Ser Asp Gly Ala Asp Leu Leu Thr Lys Leu Leu Gln Phe Glu Gly
159                               420                               425                               430
161 cga aat cgg atc tcc gca gag gat gcc atg aaa cat cca ttc ttc ctc      1464
162 Arg Asn Arg Ile Ser Ala Glu Asp Ala Met Lys His Pro Phe Phe Leu
163                               435                               440                               445
165 agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc ata ttt      1512
166 Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser Ile Phe
167                               450                               455                               460
169 gca cta aag gag att cag cta caa aag gag gcc agc ctt cgg tct tcg      1560
170 Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg Ser Ser
171                               465                               470                               475
173 tcg atg cct gac tca ggc agg cca gct ttc cgc gtg gtg gac acc gag      1608
174 Ser Met Pro Asp Ser Gly Arg Pro Ala Phe Arg Val Val Asp Thr Glu
175 480                               485                               490                               495
177 ttc taa gccacagacc gaggccccag caggcagcgg ctggaggggat gccacacccc      1664
178 Phe
181 tcacagggca gcccccaact acatcttccc tgcttactct ctgcctacct gcctgagcca      1724
183 tggtcacctg cccacttgtc c
184                               1745
186 <210> SEQ ID NO: 4
187 <211> LENGTH: 15
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
193 <223> OTHER INFORMATION: PCR Primer
195 <400> SEQUENCE: 4
196 aggttgctcg cgcgc
199 <210> SEQ ID NO: 5
200 <211> LENGTH: 22
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
206 <223> OTHER INFORMATION: PCR Primer
208 <400> SEQUENCE: 5

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## RAW SEQUENCE LISTING

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209 acagctgccg tttgatcttc tt                22
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 19
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Probe
221 <400> SEQUENCE: 6
222 cccgccgata gccatggat                19
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 19
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
232 <223> OTHER INFORMATION: PCR Primer
234 <400> SEQUENCE: 7
235 gaaggtgaag gtcggagtc                19
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
247 <400> SEQUENCE: 8
248 gaagatgggtg atgggatttc                20
251 <210> SEQ ID NO: 9
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
258 <223> OTHER INFORMATION: PCR Probe
260 <400> SEQUENCE: 9
261 caagcttccc gttctcagcc                20
264 <210> SEQ ID NO: 10
265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
271 <223> OTHER INFORMATION: Antisense Oligonucleotide
273 <400> SEQUENCE: 10
274 ctgtccatcc tttacgctgc                20
277 <210> SEQ ID NO: 11
278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
284 <223> OTHER INFORMATION: Antisense Oligonucleotide
286 <400> SEQUENCE: 11
287 ctgcattcct gtccatcctt                20

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Input Set : A:\PTO.AMC.txt

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290 <210> SEQ ID NO: 12
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
297 <223> OTHER INFORMATION: Antisense Oligonucleotide
299 <400> SEQUENCE: 12
300 ctcctgccta cctctgcatt                20
303 <210> SEQ ID NO: 13
304 <211> LENGTH: 20
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
310 <223> OTHER INFORMATION: Antisense Oligonucleotide
312 <400> SEQUENCE: 13
313 gctggtcctc ctgcctacct                20
316 <210> SEQ ID NO: 14
317 <211> LENGTH: 20
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
323 <223> OTHER INFORMATION: Antisense Oligonucleotide
325 <400> SEQUENCE: 14
326 tcagcagtca cactgctggt                20
329 <210> SEQ ID NO: 15
330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
336 <223> OTHER INFORMATION: Antisense Oligonucleotide
338 <400> SEQUENCE: 15
339 cctgggtttc agcagtcaca                20
342 <210> SEQ ID NO: 16
343 <211> LENGTH: 20
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
349 <223> OTHER INFORMATION: Antisense Oligonucleotide
351 <400> SEQUENCE: 16
352 tcatccgatc catggcgatc                20
355 <210> SEQ ID NO: 17
356 <211> LENGTH: 20
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence
360 <220> FEATURE:
362 <223> OTHER INFORMATION: Antisense Oligonucleotide
364 <400> SEQUENCE: 17
365 ttgatcttct tcatccgatc                20
368 <210> SEQ ID NO: 18

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/017,621

DATE: 01/10/2002

TIME: 20:06:06

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01102002\J017621.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date